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Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: Wed Oct 10 15:59:42 EDT 2007
=====

Reviewer Comments:

<210> 26

<211> 47

<212> RNA

<213> Artificial Sequence

<220>

<223> C10orf3 siRNA having hairpin structure

<220>

<221> misc_structure

<222> (1)...(19)

<223> C10orf3 siRNA oligonucleotide target sequence, [A]

<220>

<221> misc_structure

<222> (20)...(28)

<223> preferable loop sequence, [B]

<220>

<221> misc_structure

<222> (29)...(47)

<223> C10orf3 siRNA oligonucleotide target sequence
complementary sequence, [A']

<400> 26

ggagagactg aaaacagagu ucaagagacu cuguuuucag ucucucc

47

The above <212> response is "RNA." However, a "t" is shown in the above sequence at location 9. No "t's" are allowed in an RNA sequence. For a

combined DNA/RNA sequence, use <212> DNA, and explain in the <220>-<223> section that it is a combined DNA/RNA sequence.

<210> 27

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> poly dT-12-18 primer

<221> modified_base

<222> (13)...(18)

<223> t or absent

<400> 27

ttttttttttt tttttttt

10

The above cumulative total of "10" is incorrect: 18 nucleotides are shown in this sequence.

Application No: 10589594

Version No: 1.0

Input Set:

Output Set:

Started: 2007-09-20 09:48:00.065

Finished: 2007-09-20 09:48:01.654

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 589 ms

Total Warnings: 25

Total Errors: 2

No. of SeqIDs Defined: 27

Actual SeqID Count: 27

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)

Input Set:

Output Set:

Started: 2007-09-20 09:48:00.065
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Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 256	't' found in RNA; POS (9) SEQID(26)
E 254	The total number of bases conflicts with running total, Input: 10, Calculated : 18 SEQID(27)

SEQUENCE LISTING

<110> Nakamura, Yusuke
Furukawa, Yoichi
Oncotherapy Science, Inc.

<120> Method for Diagnosing Colorectal Cancers

<130> 082368-008900US

<140> 10589594

<141> 2007-09-20

<150> WO PCT/JP04/02145

<151> 2004-02-24

<160> 27

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2624

<212> DNA

<213> Homo sapiens

<220>

<223> C10orf3

<220>

<221> CDS

<222> (294)...(1688)

<223> C10orf3

<400> 1

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gcgaccgcgg aggggtggcga ggggcggcca ggaccgcag ccccggggcc gggccggtcc 120
ggaccgccag ggagggcagg tcagtgggca gatcgcgtcc gcgggattca atctctgcc 180
gctctgataa cagtcctttt ccctggcgct cacttcgtgc ctggcaccgc gctgggcgcc 240
tcaagaccgt tgtctcttcg atcgtttctt tggacttggc gaccatttca gag atg 296
                                         Met
                                         1
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tct tcc aga agt acc aaa gat tta att aaa agt aag tgg gga tcg aag 344
Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys
      5              10              15
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cct agt aac tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa 392
Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu
      20              25              30
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att gca cac tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga 440
Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly
      35              40              45
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aag ctg act gat aaa gag aga cac aga ctt ttg gag aaa att cga gtc 488
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Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg Val	
50 55 60 65	
ctt gag gct gag aag gag aag aat gct tat caa ctc aca gag aag gac	536
Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys Asp	
70 75 80	
aaa gaa ata cag cga ctg aga gac caa ctg aag gcc aga tat agt act	584
Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr	
85 90 95	
acc gca ttg ctt gaa cag ctg gaa gag aca acg aga gaa gga gaa agg	632
Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu Arg	
100 105 110	
agg gag cag gtg ttg aaa gcc tta tct gaa gag aaa gac gta ttg aaa	680
Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu Lys	
115 120 125	
caa cag ttg tct gct gca acc tca cga att gct gaa ctt gaa agc aaa	728
Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser Lys	
130 135 140 145	
acc aat aca ctc cgt tta tca cag act gtg gct cca aac tgc ttc aac	776
Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe Asn	
150 155 160	
tca tca ata aat aat att cat gaa atg gaa ata cag ctg aaa gat gct	824
Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp Ala	
165 170 175	
ctg gag aaa aat cag cag tgg ctc gtg tat gat cag cag cgg gaa gtc	872
Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu Val	
180 185 190	
tat gta aaa gga ctt tta gca aag atc ttt gag ttg gaa aag aaa acg	920
Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys Thr	
195 200 205	
gaa aca gct gct cat tca ctc cca cag cag aca aaa aag cct gaa tca	968
Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu Ser	
210 215 220 225	
gaa ggt tat ctt caa gaa gag aag cag aaa tgt tac aac gat ctc ttg	1016
Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu Leu	
230 235 240	
gca agt gca aaa aaa gat ctt gag gtt gaa cga caa acc ata act cag	1064
Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr Gln	
245 250 255	
ctg agt ttt gaa ctg agt gaa ttt cga aga aaa tat gaa gaa acc caa	1112
Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr Gln	
260 265 270	
aaa gaa gtt cac aat tta aat cag ctg ttg tat tca caa aga agg gca	1160
Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg Ala	

275	280	285	
gat gtg caa cat ctg gaa gat gat agg cat aaa aca gag aag ata caa			1208
Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile Gln			
290	295	300	305
aaa ctc agg gaa gag aat gat att gct agg gga aaa ctt gaa gaa gag			1256
Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu Glu			
	310	315	320
aag aag aga tcc gaa gag ctc tta tct cag gtc cag ttt ctt tac aca			1304
Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr Thr			
	325	330	335
tct ctg cta aag cag caa gaa gaa caa aca agg gta gct ctg ttg gaa			1352
Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu Glu			
	340	345	350
caa cag atg cag gca tgt act tta gac ttt gaa aat gaa aaa ctc gac			1400
Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu Asp			
	355	360	365
cgt caa cat gtg cag cat caa ttg cat gta att ctt aag gag ctc cga			1448
Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu Arg			
370	375	380	385
aaa gca aga aat caa ata aca cag ttg gaa tcc ttg aaa cag ctt cat			1496
Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu His			
	390	395	400
gag ttt gcc atc aca gag cca tta gtc act ttc caa gga gag act gaa			1544
Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr Glu			
	405	410	415
aac aga gaa aaa gtt gcc gcc tca cca aaa agt ccc act gct gca ctc			1592
Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala Leu			
	420	425	430
aat gaa agc ctg gtg gaa tgt ccc aag tgc aat ata cag tat cca gcc			1640
Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro Ala			
435	440	445	
act gag cat cgc gat ctg ctt gtc cat gtg gaa tac tgt tca aag tag			1688
Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys			
450	455	460	
caaaataagt atttgttttg atattaaaag attcaatact gtattttctg ttagcttgtg			1748
ggcattttga attatatatt tcacattttg cataaaaactg cctatctacc tttgacactc			1808
cagcatgcta gtgaatcatg tatcttttag gctgctgtgc atttctcttg gcagtgatac			1868
ctccctgaca tggttcatca tcaggctgca atgacagaat gtggtgagca gcgtctactg			1928
agactactaa ctttttgcac tgtcaaaata cttggtgagg aaaagatagc tcaggttatt			1988
gctaattgggt taatgcacca gcaagcaaaa ttttttatgt tttgggggtt tgaaaaatca			2048
aagataatta accaaggatc ttaactgtgt tcgcattttt tatccaagca cttagaaaac			2108
ctacaatcct aattttgatg tccattgtta agagggtggtg atagatacta tttttttttt			2168
catattgtat agcggttatt agaaaagttg gggattttct tgatctttat tgctgcttac			2228
cattgaaact taaccagct gtgttcccca actctgttct gcgcacgaaa cagtatctgt			2288
ttgaggcata atcttaagtg gccacacaca atgttttctc ttatgttatc tggcagtaac			2348

tgtaacttga attacattag cacattctgc ttagctaaaa ttgttaaaat aaactttaat 2408
 aaacccatgt agccctctca ttgtattgac agtatttttag ttatttttgg cattcttaaa 2468
 gctgggcaat gtaatgatca gatctttgtt tgtctgaaca ggtattttta tacatgcttt 2528
 ttgtaaacca aaaactttta aatttcttca ggttttctaa catgcttacc actgggctac 2588
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 <212> PRT
 <213> Homo sapiens

<220>
 <223> C10orf3

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 Lys Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly
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 Glu Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys
 35 40 45
 Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg
 50 55 60
 Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys
 65 70 75 80
 Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser
 85 90 95
 Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu
 100 105 110
 Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu
 115 120 125
 Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser
 130 135 140
 Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe
 145 150 155 160
 Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp
 165 170 175
 Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu
 180 185 190
 Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys
 195 200 205
 Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu
 210 215 220
 Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu
 225 230 235 240
 Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr
 245 250 255
 Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr
 260 265 270
 Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg
 275 280 285
 Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile
 290 295 300
 Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu
 305 310 315 320
 Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr
 325 330 335

Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu
 340 345 350
 Glu Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu
 355 360 365
 Asp Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu
 370 375 380
 Arg Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu
 385 390 395 400
 His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr
 405 410 415
 Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala
 420 425 430
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 Ala Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys
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<210> 3
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 <212> DNA
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<220>
 <223> GAPDH RT-PCR amplification forward primer

<400> 3
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<210> 4
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<220>
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<400> 4
 ggtccaccac tgacacgttg 20

<210> 5
 <211> 23
 <212> DNA
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<220>
 <223> C10orf3 RT-PCR amplification forward primer

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 agagatccga agagctctta tct 23

<210> 6
 <211> 21
 <212> DNA
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<220>

<223> C10orf3 RT-PCR amplification reverse primer

<400> 6
gatgctcagt ggctggatac t 21

<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> C10orf3 gene-specific RT-PCR amplification forward primer

<400> 7
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<210> 8
<211> 27
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<220>
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<400> 8
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<210> 9
<211> 26
<212> DNA
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pET28a vector

<400> 9
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<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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pET28a vector

<400> 10
tatctcgagc tttgaacagt at 22

<210> 11
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> H1RNA gene containing promoter region genomic fragment PCR
amplification primer for siRNA plasmid vector

<400> 11
tggtagccaa gtgcaggtta ta 22

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> H1RNA gene containing promoter region genomic fragment PCR
amplification primer for siRNA plasmid vector

<400> 12
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<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> BamHI and XhoI fragment containing H1RNA PCR
amplification primer

<400> 13
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<210> 14
<211> 29
<212> DNA
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<220>
<223> BamHI and XhoI fragment containing H1RNA PCR
amplification primer

<400> 14
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<210> 15
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR amplification primer for ligated DNA template

<400> 15
tttaagcttg aagaccattt ttggaaaaaa aaaaaaaaaa aaaaaaac 47

<210> 16
<211> 34
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<220>
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<400> 16
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<210> 17
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<220>
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<210> 18
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 control plasmid psiH1BX-EGFP

<400> 18
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<210> 19
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 <212> DNA
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<220>
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 (psiH1BX-C10orf3-G)

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<400> 20
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<210> 21
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> C10orf3 siRNA oligonucleotide target sequence

 <400> 21
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 <210> 22
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> C10orf3 siRNA oligonucleotide hairpin loop structure

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 <210> 23
 <211> 488
 <212> DNA
 <213> Artificial

 <220>
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 DNA fragment insertion site

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 ccactagtaa cggccgccag tgtgctggaa ttcggettgg tagccaagtg cagggttatag 120
 ggagctgaag ggaagggggg cacagtaggt ggcatcggtc ctttctgact gcccgcctccc 180
 cgcattgccgt cccgcgatat tgagctccga acctctcgcc ctgccgccgc cgggtgctccg 240
 tcgccgccgc gccgccatgg aattcgaaacg ctgacgtcat caaccgcgtc caaggaatcg 300
 cggggccagt gtcactaggc gggaacaccc agcgcgcgtg cgccctggca ggaagatggc 360
 tgtgagggac aggggagtg cgccctgcaa tatttgcatt tcgctatgtg ttctgggaaa 420
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 tctttccc 488

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 <211> 4597
 <212> DNA
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 <220>
 <223> psiH1 BX3.0 vector plasmid sequence downstream of siRNA
 DNA fragment insertion site

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 ctataatccc agcacttttg gaggcgcagg cgggcggatc acaaggtcag gaggtcgaga 120
 ccatccaggc taacacggtg aaaccccccc ccatctctac taaaaaaaaa aaatacaaaa 180
 aattagccat tagccgggcg tgggtggcgg cgctataat cccagctact tgggaggtcg 240
 aagcagaatg gcgtgaaccc gggagggcga cgttgacgtg agccgagatc gcgccgactg 300

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